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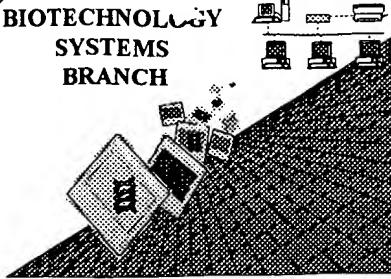
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0460
02-07-01
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RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/757,100
Source: O/P/E
Date Processed by STIC: 2/13/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/757,100</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u>Wrapped Nucleic</u>	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <u>Wrapped Aminos</u>	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <u>Incorrect Line Length</u>	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <u>Misaligned Amino Acid Numbering</u>	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <u>Non-ASCII</u>	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <u>Variable Length</u>	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <u>PatentIn ver. 2.0 "bug"</u>	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <u>Skipped Sequences (OLD RULES)</u>	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <u>Skipped Sequences (NEW RULES)</u>	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <u>Use of n's or Xaa's (NEW RULES)</u>	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <u>Use of <213>Organism (NEW RULES)</u>	Sequence(s) _____ are missing this mandatory field or its response.	
12 <u>Use of <220>Feature (NEW RULES)</u>	Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <u>PatentIn ver. 2.0 "bug"</u>	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,100

DATE: 02/13/2001
TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw
Output Set: N:\CRF3\02132001\I757100.raw

**Does Not Comply
Corrected Diskette Needed**

1 <110> APPLICANT: Monia, Brett P.
2 Gaarde, William A.
3 Nero, Pamela S.
4 <120> TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
5 Expression
6 <130> FILE REFERENCE: ISPH-0533
7 <140> CURRENT APPLICATION NUMBER: US/09/757,100
8 <141> CURRENT FILING DATE: 2001-01-09
9 <150> PRIOR APPLICATION NUMBER: 09/377,310
10 <151> PRIOR FILING DATE: 1999-08-19
11 <150> PRIOR APPLICATION NUMBER: PCT/US00/18999
12 <151> PRIOR FILING DATE: 2000-07-13
13 <160> NUMBER OF SEQ ID NOS: 44
14 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

16 <210> SEQ ID NO: 1
17 <211> LENGTH: 3791
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (233)..(3391)
23 <300> PUBLICATION INFORMATION:
24 <303> JOURNAL: DNA
25 <304> VOLUME: 12
26 <305> ISSUE: 9
27 <306> PAGES: 823-830
28 <307> DATE: 1993-11
29 <308> DATABASE ACCESSION NO: L13616/Genbank
30 <309> DATABASE ENTRY DATE: 1995-01-02
31 <400> SEQUENCE: 1
E--> 32 cgaccactgt gagcccgccg cgtgaggcgt cgggaggaag cgcggctgct
33 gtcgcccagc 60 → 60
E--> 34 gccgcgccgt cgtcgctgc ctgcgttca cggcgccgag ccgcggctccg → 120
35 agcagaactg 120
E--> 36 gggctccctt gcatcttcca gttacaaatt cagtgccttc tgcagtttcc
37 ccagagctcc 180
E--> 38 tcaagaataa cggaaaggag aatatgacag ataccttagca tcttagcaaaa ta
39 atg gca 238
40 Met Ala
41 1
E--> 42 gct gct tac ctt gac ccc aac ttg aat cac aca cca aat tcg agt
43 act 286
44 Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn Ser Ser

global error
(see item 1 on Error
summary sheet)

format error

→ 60

→ 120

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W--> 45 Thr 5 10 15
 W--> 46 5 10 15
 E--> 47 aag act cac ctg ggt act ggt atg gaa cgt tct cct ggt gca atg
 48 gag 334
 49 Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly Ala Met
 W--> 50 Glu
 W--> 51 20 25 30
 E--> 52 cga gta tta aag gtc ttt cat tat ttt gaa agc aat agt gag cca
 53 acc 382
 54 Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser Glu Pro
 W--> 55 Thr
 W--> 56 35 40 45
 E--> 57 50
 E--> 58 acc tgg gcc agt att atc agg cat gga gat gct act gat gtc agg
 59 ggc 430
 60 Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp Val Arg
 W--> 61 Gly
 W--> 62 55 60 65
 E--> 63 atc att cag aag ata gtg gac agt cac aaa gta aag cat gtg gcc
 64 tgc 478
 65 Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His Val Ala
 W--> 66 Cys
 W--> 67 70 75 80
 E--> 68 tat gga ttc cgc ctc agt cac ctg cgg tca gag gag gtt cac tgg
 69 ctt 526
 70 Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val His Trp
 W--> 71 Leu
 W--> 72 85 90 95
 E--> 73 cac gtg gat atg ggc gtc tcc agt gtg agg gag aag tat gag ctt
 74 gct 574
 75 His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr Glu Leu
 W--> 76 Ala
 W--> 77 100 105 110
 E--> 78 cac cca cca gag gag tgg aaa tat gaa ttg aga att cgt tat ttg
 79 cca 622
 80 His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg Tyr Leu
 W--> 81 Pro
 W--> 82 115 120 125
 E--> 83 130
 E--> 84 aaa gga ttt cta aac cag ttt act gaa gat aag cca act ttg aat
 85 ttc 670
 86 Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr Leu Asn
 W--> 87 Phe
 W--> 88 135 140 145
 E--> 89 ttc tat caa cag gtg aag agc gat tat atg tta gag ata gct gat
 90 caa 718
 91 Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile Ala Asp
 W--> 92 Gln
 W--> 93 150 155 160

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PATENT APPLICATION: US/09/757,100 TIME: 08:09:56

Input Set : N:\CrF3\02052001\I757100.raw
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E--> 94 gtg gac cag gaa att gct ttg aag ttg ggt tgt cta gaa ata cgg
 95 cga 766
 96 Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu Ile Arg
 W--> 97 Arg
 W--> 98 165 170 175
 E--> 99 tca tac tgg gag atg cg^g ggc aat gca cta gaa aag aag tct aac
 100 tat 814
 101 Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys Ser Asn
 W--> 102 Tyr
 W--> 103 180 185 190
 E--> 104 gaa gta tta gaa aaa gat gtt ggt tta aag cga ttt ttt cct aag
 105 agt 862
 106 Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro Lys
 W--> 107 Ser
 W--> 108 195 200 205
 E--> 109 210
 E--> 110 tta ctg gat tct gtc aag gcc aaa aca cta aga aaa ctg atc caa
 111 caa 910
 112 Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile Gln
 W--> 113 Gln
 W--> 114 215 220 225
 E--> 115 aca ttt aga caa ttt gcc aac ctt aat aga gaa gaa agt att ctg
 116 aaa 958
 117 Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile Leu
 W--> 118 Lys
 W--> 119 230 235 240
 E--> 120 ttc ttt gag atc ctg tct cca gtc tac aga ttt gat aag gaa tgc
 121 ttc 1006
 122 Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys
 W--> 123 Phe
 W--> 124 245 250 255
 E--> 125 aag tgt gct ctt ggt tca agc tgg att att tca gtg gaa ctg gca
 126 atc 1054
 127 Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu Ala
 W--> 128 Ile
 W--> 129 260 265 270
 E--> 130 ggc cca gaa gaa gga atc agt tac cta acg gac aag ggc tgc aat
 131 ccc 1102
 132 Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn
 W--> 133 Pro
 W--> 134 275 280 285
 E--> 135 290
 E--> 136 aca cat ctt gct gac ttc act caa gtg caa acc att cag tat tca
 137 aac 1150
 138 Thr His Leu Ala Asp Phe Thr Asn Gln Val Gln Thr Ile Gln Tyr Ser
 W--> 139 Asn
 W--> 140 295 300 305
 E--> 141 agt gaa gac aag gac aga aaa gga atg cta caa cta aaa ata gca
 142 agt 1198

sane

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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

143 Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala
 W--> 144 Gly 310 315 320
 W--> 145 gca ccc gag cct ctg aca gtg acg gca cca tcc cta acc att gcg
 E--> 146 147 gag 1246
 148 Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile Ala
 W--> 149 Glu 325 330 335
 W--> 150 E--> 151 152 aat atg gct gac cta ata gat ggg tac tgc cgg ctg gtg aat gga
 acc 1294
 153 Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn Gly
 W--> 154 Thr 340 345 350
 W--> 155 E--> 156 157 tcg cag tca ttt atc atc aga cct cag aaa gaa ggt gaa cgg gct
 ttg 1342
 158 Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg Ala
 W--> 159 Leu 355 360 365
 W--> 160 E--> 161 370
 E--> 162 163 cca tca ata cca aag ttg gcc aac agc gaa aag caa ggc atg cgg
 aca 1390
 164 Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met Arg
 W--> 165 Thr 375 380 385
 W--> 166 E--> 167 168 cac gcc gtc tct gtg tca gaa aca gat gat tat gct gag att ata
 gat 1438
 169 His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile Ile
 W--> 170 Asp 390 395 400
 W--> 171 E--> 172 173 gaa gaa gat act tac acc atg ccc tca acc agg gat tat gag att
 caa 1486
 174 Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu Ile
 W--> 175 Gln 405 410 415
 W--> 176 E--> 177 178 aga gaa aga ata gaa ctt gga cga tgt att gga gaa ggc caa ttt
 gga 1534
 179 Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln Phe
 W--> 180 Gly 420 425 430
 W--> 181 E--> 182 183 gat gta cat caa ggc att tat atg agt cca gag aat cca gct ttg
 gcg 1582
 184 Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala Leu
 W--> 185 Ala 435 440 445
 W--> 186 E--> 187 450
 E--> 188 189 gtt gca att aaa aca tgt aaa aac tgt act tcg gac agc gtg aga
 gag 1630
 190 Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val Arg
 Glu 191

Manne

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Input Set : N:\Crf3\02052001\I757100.raw
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W--> 192 455 460 465
 E--> 193 aaa ttt ctt caa gaa gcc tta aca atg cgt cag ttt gac cat cct
 194 cat 1678
 195 Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp His Pro
 W--> 196 His
 W--> 197 470 475 480
 E--> 198 att gtg aag ctg att gga gtc atc aca gag aat cct gtc tgg ata
 199 atc 1726
 200 Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp Ile
 W--> 201 Ile
 W--> 202 485 490 495
 E--> 203 atg gag ctg tgc aca ctt gga gag ctg agg tca ttt ttg caa gta
 204 agg 1774
 205 Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln Val
 W--> 206 Arg
 W--> 207 500 505 510
 E--> 208 aaa tac agt ttg gat cta gca tct ttg atc ctg tat gcc tat cag
 209 ctt 1822
 210 Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr Gln
 W--> 211 Leu
 W--> 212 515 520 525
 E--> 213 530
 E--> 214 agt aca gct ctt gca tat cta gag agc aaa aga ttt gta cac agg
 215 gac 1870
 216 Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His Arg
 W--> 217 Asp
 W--> 218 535 540 545
 E--> 219 att gct gct cgg aat gtt ctg gtg tcc tca aat gat tgt gta aaa
 220 tta 1918
 221 Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val Lys
 W--> 222 Leu
 W--> 223 550 555 560
 E--> 224 gga gac ttt gga tta tcc cga tat atg gaa gat agt act tac tac
 225 aaa 1966
 226 Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr Tyr
 W--> 227 Lys
 W--> 228 565 570 575
 E--> 229 gct tcc aaa gga aaa ttg cct att aaa ttg atg gct cca gag tca
 230 atc 2014
 231 Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu Ser
 W--> 232 Ile
 W--> 233 580 585 590
 E--> 234 aat ttt cga cgt ttt acc tca gct agt gac gta ttg atg ttt ggt
 235 gtg 2062
 236 Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe Gly
 W--> 237 Val
 W--> 238 595 600 605
 E--> 239 610
 E--> 240 tgt atg ttg gag ata ctg atg cat ggt gtg aag cct ttt caa gga

panel

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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

241 gtg 2110
 242 Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln Gly
 W--> 243 Val
 W--> 244 615 620 625
 E--> 245 aag aac aat gat gta atc ggt cga att gaa aat ggg gaa aga tta
 246 cca 2158
 247 Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg Leu
 W--> 248 Pro
 W--> 249 630 635 640
 E--> 250 atg cct cca aat tgt cct cct acc ctc tac agc ctt atg acg aaa
 251 tgc 2206
 252 Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr Lys
 W--> 253 Cys
 W--> 254 645 650 655
 E--> 255 tgg gcc tat gac ccc agc agg cgg ccc agg ttt act gaa ctt aaa
 256 gct 2254
 257 Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys
 W--> 258 Ala
 W--> 259 660 665 670
 E--> 260 cag ctc agc aca atc ctg gag gaa gag aag gct cag caa gaa gag
 261 cgc 2302
 262 Gln Leu Ser Thr Ile Leu Glu Glu Lys Ala Gln Gln Glu Glu
 W--> 263 Arg
 W--> 264 675 680 685
 E--> 265 690
 E--> 266 atg agg atg gag tcc aga aga cag gcc aca gtg tcc tgg gac tcc
 267 gga 2350
 268 Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp Asp Ser
 W--> 269 Gly
 W--> 270 695 700 705
 E--> 271 ggg tct gat gaa gca ccg ccc aag ccc agc aga ccg ggt tat ccc
 272 agt 2398
 273 Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly Tyr Pro
 W--> 274 Ser
 W--> 275 710 715 720
 E--> 276 ccg agg tcc agc gaa gga ttt tat ccc agc cca cag cac atg gta
 277 caa 2446
 278 Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His Met Val
 W--> 279 Gln
 W--> 280 725 730 735
 E--> 281 acc aat cat tac cag gtt tct ggc tac cct ggt tca cat gga atc
 282 aca 2494
 283 Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His Gly Ile
 W--> 284 Thr
 W--> 285 740 745 750
 E--> 286 gcc atg gct ggc agc atc tat cca ggt cag gca tct ctt ttg gac
 287 caa 2542
 288 Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu Leu Asp
 Gln
 W--> 289

same

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,100

DATE: 02/13/2001
TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw
Output Set: N:\CRF3\02132001\I757100.raw

W--> 290	755	760	765
E--> 291	770		
E--> 292	aca gat tca tgg aat cat aga cct cag gag ata gca atg tgg cag		
293	ccc 2590		
294	Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met Trp Gln		
W--> 295	Pro		
W--> 296	775	780	785
E--> 297	aat gtg gag gac tct aca gta ttg gac ctg cga ggg att ggg caa		
298	gtg 2638		
299	Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile Gly Gln		
W--> 300	Val		
W--> 301	790	795	800
E--> 302	ttg cca acc cat ctg atg gaa gag cgt cta atc cga cag caa cag		
303	gaa 2686		
304	Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln Gln		
W--> 305	Glu		
W--> 306	805	810	815
E--> 307	atg gaa gaa gat cag cgc tgg ctg gaa aaa gag gaa aga ttt ctg		
308	aaa 2734		
309	Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg Phe Leu		
W--> 310	Lys		
W--> 311	820	825	830
E--> 312	cct gat gtg aga ctc tct cga ggc agt att gac agg gag gat gga		
313	agt 2782		
314	Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu Asp Gly		
W--> 315	Ser		
W--> 316	835	840	845
E--> 317	850		
E--> 318	ctt cag ggt ccg att gga aaccaa cat ata tat cag cct gtg ggt		
319	aaa 2830		
320	Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro Val Gly		
W--> 321	Lys		
W--> 322	855	860	865
E--> 323	cca gat cct gca gct cca cca aag aaa ccg cct cgc cct gga gct		
324	ccc 2878		
325	Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro Gly Ala		
W--> 326	Pro		
W--> 327	870	875	880
E--> 328	ggt cat ctg gga agc ctt gcc agc ctc agc agc cct gct gac agc		
329	tac 2926		
330	Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala Asp Ser		
W--> 331	Tyr		
W--> 332	885	890	895
E--> 333	aac gag ggt gtc aag ctt cag ccc cag gaa atc agc ccc cct cct		
334	act 2974		
335	Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro Pro Pro		
W--> 336	Thr		
W--> 337	900	905	910
E--> 338	gcc aac ctg gac cgg tcg aat gat aag gtg tac gag aat gtg acg		

Park

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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

339 ggc 3022
 340 Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn Val Thr
 W--> 341 Gly
 W--> 342 915 920 925
 E--> 343 930
 E--> 344 ctg gtg aaa gct gtc atc gag atg tcc agt aaa atc cag cca gcc
 345 cca 3070
 346 Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln Pro Ala
 W--> 347 Pro
 W--> 348 935 940 945
 E--> 349 cca gag gag tat gtc cct atg gtg aag gaa gtc ggc ttg gcc ctg
 350 agg 3118
 351 Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu Ala Leu
 W--> 352 Arg
 W--> 353 950 955 960
 E--> 354 aca tta ttg gcc act gtg gat gag acc att ccc ctc cta cca gcc
 355 agc 3166
 356 Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu Pro Ala
 W--> 357 Ser
 W--> 358 965 970 975
 E--> 359 acc cac cga gag att gag atg gca cag aag cta ttg aac tct gac
 360 ctg 3214
 361 Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn Ser Asp
 W--> 362 Leu
 W--> 363 980 985 990
 E--> 364 ggt gag ctc atc aac aag atg aaa ctg gcc cag cag tat gtc atg
 365 acc 3262
 366 Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr Val Met
 W--> 367 Thr
 W--> 368 995 1000 1005
 E--> 369 1010
 E--> 370 agc ctc cag caa gag tac aaa aag caa atg ctg act gct gct cac
 371 gcc 3310
 372 Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala Ala His
 W--> 373 Ala
 W--> 374 1015 1020 1025
 E--> 375 ctg gct gtg gat gcc aaa aac tta ctc gat gtc att gac caa gca
 376 aga 3358
 377 Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp Gln Ala
 W--> 378 Arg
 W--> 379 1030 1035 1040
 E--> 380 ctg aaa atg ctt ggg cag acg aga cca cac tga gcctccctta
 381 ggagcacgtc 3411
 382 Leu Lys Met Leu Gly Gln Thr Arg Pro His
 W--> 383 1045 1050
 E--> 384 ttgctaccct ctttgaaga tgttctctag cttccacca gcagcgagga
 385 attaacccctg 3471
 E--> 386 tgtccctcagt cgccagcact tacagctcca acttttttga atgaccatct
 387 ggttgaaaaaa 3531

Done

RAW SEQUENCE LISTING DATE: 02/13/2001
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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

```

E--> 388 tctttctcat ataagttaa ccacacttgc atttgggttc attttttgtt
  389 ttgtttttt 3591
E--> 390 caatcatgat attcagaaaa atccaggatc caaaatgtgg cgtttttcta
  391 agaatgaaaa 3651
E--> 392 ttatatgtaa gcttttaagc atcatgaaga acaattttagt ttcacattaa
  393 gatacggtct 3711
E--> 394 aaagggggat ggccaagggg tgacatctta attcctaaac taccttagct
  395 gcatagtgg 3771
E--> 396 agaggagagc tagaagcaaa
  397
  399 <210> SEQ ID NO: 2
  400 <211> LENGTH: 1052
  401 <212> TYPE: PRT
  402 <213> ORGANISM: Homo sapiens
  403 <400> SEQUENCE: 2
  404 Met Ala Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn
E--> 405 Ser
  406      1          5          10          15
  407 Ser Thr Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly
E--> 408 Ala
  409      20         25         30
  410 Met Glu Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser
E--> 411 Glu
  412      35         40         45
  413 Pro Thr Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp
E--> 414 Val
  415      50         55         60
  416 Arg Gly Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His
E--> 417 Val
  418      65         70         75
  419
  420 Ala Cys Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val
E--> 421 His
  422      85         90         95
  423 Trp Leu His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr
E--> 424 Glu
  425      100        105        110
  426 Leu Ala His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg
E--> 427 Tyr
  428      115        120        125
  429 Leu Pro Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr
E--> 430 Leu
  431      130        135        140
  432 Asn Phe Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile
E--> 433 Ala
  434      145        150        155
  435      160
  436 Asp Gln Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu
E--> 437 Ile

```

All item 2

on Error Summary
Sheet

RAW SEQUENCE LISTING DATE: 02/13/2001
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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

E--> 438 165 170 175
 439 Arg Arg Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys
 E--> 440 Ser
 E--> 441 180 185 190
 442 Asn Tyr Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe
 E--> 443 Pro
 E--> 444 195 200 205
 445 Lys Ser Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu
 E--> 446 Ile
 E--> 447 210 215 220
 448 Gln Gln Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser
 Ile
 E--> 449
 E--> 450 225 230 235
 E--> 451 240
 452 Leu Lys Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys
 E--> 453 Glu
 E--> 454 245 250 255
 455 Cys Phe Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu
 Leu
 E--> 456
 E--> 457 260 265 270
 458 Ala Ile Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly
 Cys
 E--> 459
 E--> 460 275 280 285
 461 Asn Pro Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln
 Tyr
 E--> 462
 E--> 463 290 295 300
 464 Ser Asn Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys
 Ile
 E--> 465
 E--> 466 305 310 315
 E--> 467 320
 468 Ala Gly Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr
 Ile
 E--> 469
 E--> 470 325 330 335
 471 Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val
 Asn
 E--> 472
 E--> 473 340 345 350
 474 Gly Thr Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu
 Arg
 E--> 475
 E--> 476 355 360 365
 477 Ala Leu Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly
 Met
 E--> 478
 E--> 479 370 375 380
 480 Arg Thr His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu
 Ile
 E--> 481
 E--> 482 385 390 395
 E--> 483 400
 484 Ile Asp Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr
 Glu
 E--> 485
 E--> 486 405 410 415

*Parse
Error*

RAW SEQUENCE LISTING DATE: 02/13/2001
 PATENT APPLICATION: US/09/757,100 TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

487 Ile Gln Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly
 E--> 488 Gln
 E--> 489 420 425 430
 490 Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro
 E--> 491 Ala
 E--> 492 435 440 445
 493 Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser
 E--> 494 Val
 E--> 495 450 455 460
 496 Arg Glu Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp
 E--> 497 His
 E--> 498 465 470 475
 E--> 499 480
 500 Pro His Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val
 E--> 501 Trp
 E--> 502 485 490 495
 503 Ile Ile Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu
 E--> 504 Gln
 E--> 505 500 505 510
 506 Val Arg Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala
 E--> 507 Tyr
 E--> 508 515 520 525
 509 Gln Leu Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val
 E--> 510 His
 E--> 511 530 535 540
 512 Arg Asp Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys
 E--> 513 Val
 E--> 514 545 550 555
 E--> 515 560
 516 Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr
 E--> 517 Tyr
 E--> 518 565 570 575
 519 Tyr Lys Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro
 E--> 520 Glu
 E--> 521 580 585 590
 522 Ser Ile Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met
 E--> 523 Phe
 E--> 524 595 600 605
 525 Gly Val Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe
 E--> 526 Gln
 E--> 527 610 615 620
 528 Gly Val Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu
 E--> 529 Arg
 E--> 530 625 630 635
 E--> 531 640
 532 Leu Pro Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met
 E--> 533 Thr
 E--> 534 645 650 655
 535 Lys Cys Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu

Maree

RAW SEQUENCE LISTING DATE: 02/13/2001
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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

E--> 536 Leu
 E--> 537 660 665 670
 538 Lys Ala Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln
 E--> 539 Glu
 E--> 540 675 680 685
 541 Glu Arg Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp
 E--> 542 Asp
 E--> 543 690 695 700
 544 Ser Gly Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly
 E--> 545 Tyr
 E--> 546 705 710 715
 E--> 547 720
 548 Pro Ser Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His
 E--> 549 Met
 E--> 550 725 730 735
 551 Val Gln Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His
 E--> 552 Gly
 E--> 553 740 745 750
 554 Ile Thr Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu
 E--> 555 Leu
 E--> 556 755 760 765
 557 Asp Gln Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met
 E--> 558 Trp
 E--> 559 770 775 780
 560 Gln Pro Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile
 E--> 561 Gly
 E--> 562 785 790 795
 E--> 563 800
 564 Gln Val Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln
 E--> 565 Gln
 E--> 566 805 810 815
 567 Gln Glu Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg
 E--> 568 Phe
 E--> 569 820 825 830
 570 Leu Lys Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu
 E--> 571 Asp
 E--> 572 835 840 845
 573 Gly Ser Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro
 E--> 574 Val
 E--> 575 850 855 860
 576 Gly Lys Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro
 E--> 577 Gly
 E--> 578 865 870 875
 E--> 579 880
 580 Ala Pro Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala
 E--> 581 Asp
 E--> 582 885 890 895
 583 Ser Tyr Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro
 E--> 584 Pro

name

RAW SEQUENCE LISTING
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TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw
Output Set: N:\CRF3\02132001\I757100.raw

E--> 585 900 905 910
586 Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn
E--> 587 Val
E--> 588 915 920 925
589 Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln
E--> 590 Pro
E--> 591 930 935 940
592 Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu
E--> 593 Ala
E--> 594 945 950 955
E--> 595 960
596 Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu
E--> 597 Pro
E--> 598 965 970 975
599 Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn
E--> 600 Ser
E--> 601 980 985 990
602 Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr
E--> 603 Val
E--> 604 995 1000 1005
605 Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala
E--> 606 Ala
E--> 607 1010 1015 1020
608 His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp
E--> 609 Gln
E--> 610 025 1030 1035
E--> 611 1040
612 Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His
E--> 613 1045 1050
615 <210> SEQ ID NO: 3
616 <211> LENGTH: 20
617 <212> TYPE: DNA
618 <213> ORGANISM: Artificial Sequence
619 <220> FEATURE:
620 <223> OTHER INFORMATION: antisense sequence
621 <400> SEQUENCE: 3
E--> 622 ccgcgggctc acagtggtcg
623 20
625 <210> SEQ ID NO: 4
626 <211> LENGTH: 20
627 <212> TYPE: DNA
628 <213> ORGANISM: Artificial Sequence
629 <220> FEATURE:
630 <223> OTHER INFORMATION: antisense sequence
631 <400> SEQUENCE: 4
E--> 632 ggccgcgtga agcgaaggca
633 20
635 <210> SEQ ID NO: 5
636 <211> LENGTH: 20

same

*see item 1
on even
summary sheet*

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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

637 <212> TYPE: DNA
 638 <213> ORGANISM: Artificial Sequence
 639 <220> FEATURE:
 640 <223> OTHER INFORMATION: antisense sequence
 641 <400> SEQUENCE: 5
 E--> 642 cagttctgct cgggaccgcgg
 643 20
 645 <210> SEQ ID NO: 6
 646 <211> LENGTH: 20
 647 <212> TYPE: DNA
 648 <213> ORGANISM: Artificial Sequence
 649 <220> FEATURE:
 650 <223> OTHER INFORMATION: antisense sequence
 651 <400> SEQUENCE: 6
 E--> 652 gaaactgcag aaggcactga
 653 20
 655 <210> SEQ ID NO: 7
 656 <211> LENGTH: 20
 657 <212> TYPE: DNA
 658 <213> ORGANISM: Artificial Sequence
 659 <220> FEATURE:
 660 <223> OTHER INFORMATION: antisense sequence
 661 <400> SEQUENCE: 7
 E--> 662 ttctcccttc cgttattctt
 663 20
 665 <210> SEQ ID NO: 8
 666 <211> LENGTH: 20
 667 <212> TYPE: DNA
 668 <213> ORGANISM: Artificial Sequence
 669 <220> FEATURE:
 670 <223> OTHER INFORMATION: antisense sequence
 671 <400> SEQUENCE: 8
 E--> 672 ctagatgcta ggtatctgtc
 673 20
 675 <210> SEQ ID NO: 9
 676 <211> LENGTH: 20
 677 <212> TYPE: DNA
 678 <213> ORGANISM: Artificial Sequence
 679 <220> FEATURE:
 680 <223> OTHER INFORMATION: antisense sequence
 681 <400> SEQUENCE: 9
 E--> 682 ttttgctaga tgctaggtat
 683 20
 685 <210> SEQ ID NO: 10
 686 <211> LENGTH: 20
 687 <212> TYPE: DNA
 688 <213> ORGANISM: Artificial Sequence
 689 <220> FEATURE:
 690 <223> OTHER INFORMATION: antisense sequence

same

RAW SEQUENCE LISTING DATE: 02/13/2001
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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

691 <400> SEQUENCE: 10
 E--> 692 ggttaagcagc tgccattatt
 693 20
 695 <210> SEQ ID NO: 11
 696 <211> LENGTH: 20
 697 <212> TYPE: DNA
 698 <213> ORGANISM: Artificial Sequence
 699 <220> FEATURE:
 700 <223> OTHER INFORMATION: antisense sequence
 701 <400> SEQUENCE: 11
 E--> 702 agtaccagg tgagtcttag
 703 20
 705 <210> SEQ ID NO: 12
 706 <211> LENGTH: 20
 707 <212> TYPE: DNA
 708 <213> ORGANISM: Artificial Sequence
 709 <220> FEATURE:
 710 <223> OTHER INFORMATION: antisense sequence
 711 <400> SEQUENCE: 12
 E--> 712 cctgacatca gtagcatctc
 713 20
 715 <210> SEQ ID NO: 13
 716 <211> LENGTH: 20
 717 <212> TYPE: DNA
 718 <213> ORGANISM: Artificial Sequence
 719 <220> FEATURE:
 720 <223> OTHER INFORMATION: antisense sequence
 721 <400> SEQUENCE: 13
 E--> 722 gttggcttat cttcagtaaa
 723 20
 725 <210> SEQ ID NO: 14
 726 <211> LENGTH: 20
 727 <212> TYPE: DNA
 728 <213> ORGANISM: Artificial Sequence
 729 <220> FEATURE:
 730 <223> OTHER INFORMATION: antisense sequence
 731 <400> SEQUENCE: 14
 E--> 732 ggtagggat ggtgcgtca
 733 20
 735 <210> SEQ ID NO: 15
 736 <211> LENGTH: 20
 737 <212> TYPE: DNA
 738 <213> ORGANISM: Artificial Sequence
 739 <220> FEATURE:
 740 <223> OTHER INFORMATION: antisense sequence
 741 <400> SEQUENCE: 15
 E--> 742 tggggtttc caatcgacc
 743 20
 745 <210> SEQ ID NO: 16

Name

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Input Set : N:\Crf3\02052001\I757100.raw
 Output Set: N:\CRF3\02132001\I757100.raw

746 <211> LENGTH: 20
 747 <212> TYPE: DNA
 748 <213> ORGANISM: Artificial Sequence
 749 <220> FEATURE:
 750 <223> OTHER INFORMATION: antisense sequence
 751 <400> SEQUENCE: 16
 E--> 752 ctagggagg ctcaagtgtgg
 753 20
 755 <210> SEQ ID NO: 17
 756 <211> LENGTH: 20
 757 <212> TYPE: DNA
 758 <213> ORGANISM: Artificial Sequence
 759 <220> FEATURE:
 760 <223> OTHER INFORMATION: antisense sequence
 761 <400> SEQUENCE: 17
 E--> 762 attcctcgct gctggtgaa
 763 20
 765 <210> SEQ ID NO: 18
 766 <211> LENGTH: 20
 767 <212> TYPE: DNA
 768 <213> ORGANISM: Artificial Sequence
 769 <220> FEATURE:
 770 <223> OTHER INFORMATION: antisense sequence
 771 <400> SEQUENCE: 18
 E--> 772 tttcaaccag atggtcattc
 773 20
 775 <210> SEQ ID NO: 19
 776 <211> LENGTH: 20
 777 <212> TYPE: DNA
 778 <213> ORGANISM: Artificial Sequence
 779 <220> FEATURE:
 780 <223> OTHER INFORMATION: antisense sequence
 781 <400> SEQUENCE: 19
 E--> 782 ttctgaatat catgattgaa
 783 20
 785 <210> SEQ ID NO: 20
 786 <211> LENGTH: 20
 787 <212> TYPE: DNA
 788 <213> ORGANISM: Artificial Sequence
 789 <220> FEATURE:
 790 <223> OTHER INFORMATION: antisense sequence
 791 <400> SEQUENCE: 20
 E--> 792 catgatgctt aaaagcttac
 793 20
 795 <210> SEQ ID NO: 21
 796 <211> LENGTH: 20
 797 <212> TYPE: DNA
 798 <213> ORGANISM: Artificial Sequence
 799 <220> FEATURE:

same

RAW SEQUENCE LISTING

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Input Set : N:\Crf3\02052001\I757100.raw
Output Set: N:\CRF3\02132001\I757100.raw

name

800 <223> OTHER INFORMATION: antisense sequence
801 <400> SEQUENCE: 21
E--> 802 aatgtgaaca
803 20

taaatttttc

FYI; Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 02/13/2001
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Input Set : N:\Crf3\02052001\I757100.raw
Output Set: N:\CRF3\02132001\I757100.raw

L:32 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:140 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

VERIFICATION SUMMARY DATE: 02/13/2001
PATENT APPLICATION: US/09/757,100 TIME: 08:09:57

Input Set : N:\Crf3\02052001\I757100.raw
Output Set: N:\CRF3\02132001\I757100.raw

L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:405 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:622 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:3
L:632 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:4
L:642 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:5
L:652 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:6
L:662 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:7
L:672 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:8
L:682 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:9
L:692 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:10
L:702 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:11
L:712 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
L:722 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:13
L:732 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:14
L:742 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:15
L:752 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:16
L:762 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:17
L:772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:18
L:782 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:19
L:792 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:20
L:802 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:21
L:812 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:22
L:822 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:23
L:832 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:24
L:842 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:25
L:852 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:26
L:862 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:27
L:872 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:28
L:882 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:29
L:892 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:30
L:902 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:31
L:912 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:32
L:922 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:33
L:932 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:34
L:942 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:35
L:952 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:36
L:962 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:37
L:972 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:38
L:982 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:39
L:992 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:40
L:1002 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:41
L:1012 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:42
L:1022 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:43
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1034 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:44